## SEQUENCE LISTING

<110> Koelsch, Gerald Tang, Jordan J. N. Hong, Lin Ghosh, Arun K. The Board of Trustees of the University of Illinois Oklahoma Medical Research Foundation <120> Inhibitors of Memapsin 2 and Use Thereof <130> 022266-000930US <140> US 10/773,754 <141> 2004-02-06 <150> US 60/141,363 <151> 1999-06-28 <150> US 60/168,060 <151> 1999-11-30 <150> US 60/177,836 <151> 2000-01-25 <150> US 60/178,368 <151> 2000-01-27 <150> US 60/210,292 <151> 2000-06-08 <150> US 09/603,713 <151> 2000-06-27 <150> US 09/845,226 <151> 2001-04-30 <160> 39 <170> PatentIn Ver. 2.1 <210> 1 <211> 3252 <212> DNA <213> Homo sapiens <220> <223> memapsin 2 <400> 1 gegggagtge tgeetgeeca eggeacecag caeggeatee ggetgeecet gegeagegge 60 ctggggggcg ccccctggg gctgcggctg ccccgggaga ccgacgaaga gcccgaggag 120 cccggccgga ggggcagctt tgtggagatg gtggacaacc tgaggggcaa gtcggggcag 180 ggctactacg tggagatgac cgtgggcagc ccccgcaga cgctcaacat cctggtggat 240 acaggcagca gtaactttgc agtgggtgct gcccccacc ccttcctgca tcgctactac 300 cagaggcagc tgtccagcac ataccgggac ctccggaagg gtgtgtatgt gccctacacc 360 cagggcaagt gggaagggga gctgggcacc gacctggtaa gcatccccca tggccccaac 420 gtcactgtgc gtgccaacat tgctgccatc actgaatcag acaagttctt catcaacggc 480 tccaactggg aaggcatcct ggggctggcc tatgctgaga ttgccaggcc tgacgactcc 540 ° ctggagcctt tctttgactc tctggtaaag cagacccacg ttcccaacct cttctccctg 600

cagctttgtg gtgctggctt cccctcaac cagtctgaag tgctggcctc tgtcggaggg 660

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ggcaccaccc cttggaacat tttcccagtc atctcactct acctaatggg tgaggttacc 1020
aaccagteet teegeateae cateetteeg cageaatace tgeggeeagt ggaagatgtg 1080
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catcccatct cagaagatgg gtgttgtttt caatgttttc ttttctgtgg ttgcagcctg 2220
accaaaagtg agatgggaag ggcttatcta gccaaagagc tcttttttag ctctcttaaa 2280
tgaagtgccc actaagaagt tccacttaac acatgaattt ctgccatatt aatttcattg 2340
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aaaaaaaaa aa
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<211> 488
<212> PRT
<213> Homo sapiens
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<223> purified memapsin 2, aspartic proteinase 2 (ASP2)
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<223> amino acids 28-48 are remnant putative propeptide residues
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<220>

<223> amino acids 54-57, 61-68, 73-80, 86-89, 109-111, 113-118, 123-134, 143-154, 165-168, 198-202, and 220-224 are N-lobe beta strands

<220>

<223> amino acids 58-61, 78, 80, 82-83, 116, 118-121, 156, 166, 174, 246, 274, 276, 278-281, 283, and 376-377 are residues in contact with the OM99-2 inhibitor

<220>

<223> amino acids 184-191 and 210-217 are N-lobe helices

<220>

<220>

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Ala Gly Val Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro
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Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg 20 25 30

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val 35 40 45

Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val 50 55 60

Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp 65 70 75 80

Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu 85 90 95

His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg 100 105 110

Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu 115 120 125

Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg 130 135 140

Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
145 150 155 160

Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg 165 170 175

Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr 180 185 190 His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro 200 Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile 215 Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val 280 Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala 315 310 Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met 330 325 Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln 345 Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr 360 Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr 420 Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val 440 Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val 450 455 Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe 475 Ala Asp Asp Ile Ser Leu Leu Lys 485

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<210> 3
<211> 503
<212> PRT
<213> Homo sapiens
<220>
<223> pro-memapsin 2
<220>
<223> amino acids 1-13 are the T7 promoter
<223> amino acids 1-15 are vector-derived residues
<223> amino acids 16-64 are a putative pro-peptide
<223> amino acids 16-456 are pro-memapsin 2 T1
<223> amino acids 16-421 are promemapsin 2 T2
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Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Ala
Gly Val Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu
                                 25
Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu
Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu
Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
    130
Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser
                165
                                    170
Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
                                185
            180
```

Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His 200 Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu 215 Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly 230 Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser 280 Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe 295 Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe 310 315 Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly 345 Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr 360 Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met 455 Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys 475 Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala 485 490 Asp Asp Ile Ser Leu Leu Lys

500

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<210> 4
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:synthetic
      peptide derived from amyloid precursor protein
      (APP) beta-secretase site
<400> 4
Ser Glu Val Lys Met Asp Ala Glu Phe Arg
<210> 5
<211> 10
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:synthetic
      peptide derived from amyloid precursor protein
      (APP) beta-secretase site containing the "Swedish
      mutation"
<400> 5
Ser Glu Val Asn Leu Asp Ala Glu Phe Arg
<210> 6
<211> 8
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:synthetic
      peptide derived from the processing site of
      presenilin 1
<400> 6
Ser Val Asn Met Ala Glu Gly Asp
 1
                  5
<210> 7
<211> 12
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:synthetic
      peptide derived from amyloid precursor protein
      (APP) gamma-secretase site
Lys Gly Gly Val Val Ile Ala Thr Val Ile Val Lys
                                      10
 1
                  5
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<210> 8
<211> 3
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:signature
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<221> MOD RES
<222> (2)
<223> Xaa = Thr or Ser
<400> 8
Asp Xaa Gly
<210> 9
<211> 8
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:synthetic
      peptide PS1-gamma in vivo beta-processing site of
      human presenilin 1, human memapsin 2 cleavage
      substrate
<400> 9
Leu Val Asn Met Ala Glu Gly Asp
<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: PCR
      amplification primer NHASPF1
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                                                                    28
ggtaagcatc ccccatggcc ccaacgtc
<210> 11
<211> 28
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: PCR
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<400> 11
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gacgttgggg ccatggggga tgcttacc
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	Artificial Sequence		
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	amplification primer NHASPF2		
	•		
-400-	10		
<400>			
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<210>	13		
<211>			
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	amplification primer NHASPR2		
	ampilitoacion primor minorm		
<400>	1 2		
		2.2	
ccaatt	cgtt ttcgggcccg atcaaagaca acg	33	
<210>	14		
<211>			
<212>			
<213>	Artificial Sequence		
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	amplification adapter primer AP1		
	umpaca and pacameters and a		
<400>	1.4		
		27	
ccatco	taat acgactcact atagggc	21	
<210>	15		
<211>	23		
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	tata gggetegage gge	23	
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<210>	16		
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<212>	DNA		
	Artificial Sequence		
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<220>	prominelon of publicial demonstration and the		
<223>	Description of Artificial Sequence:outside primer		
	CT1 OFWD		

. . . .

<400> 16 cttttgagca agttcagcct ggttaa	26
<210> 17 <211> 31 <212> DNA <213> Artificial Sequence	
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<400> 17 gaggtggctt atgagtattt cttccagggt a	31
<210> 18 <211> 22 <212> DNA <213> Artificial Sequence  <220> <223> Description of Artificial Sequence:outside primer GT11FWD	
<400> 18 tggcgacgac tcctggagcc cg	22
<210> 19 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence:outside primer	
GT11REV <400> 19 tgacaccaga ccaactggta atgg	24
<210> 20 <211> 27 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence:amplification primer PASPN1	
<400> 20 catatggcgg gagtgctgcc tgcccac	27
<210> 21 <211> 38 <212> DNA <213> Artificial Sequence	

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<223> Description of Artificial Sequence:amplification
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<211> 8
<212> PRT
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      insulin beta chain hydrolytic site #5
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<221> MOD_RES
<222> (3)
<223> Xaa = cysteic acid
<400> 22
His Leu Xaa Gly Ser His Leu Val
<210> 23
<211> 8
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:oxidized bovine
      insulin beta chain hydrolytic site #6
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<222> (1)
<223> Xaa = cysteic acid
<400> 23
Xaa Gly Glu Arg Gly Phe Phe Tyr
                  5
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<210> 24
<211> 5
<212> PRT
<213> Artificial Sequence
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      peptide NCH-gamma hydrolytic site #7
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Val Gly Ser Gly Val
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<211> 7
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence:synthetic
      peptide NCH-gamma hydrolytic site #9
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Gly Val Leu Leu Ser Arg Lys
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<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence:synthetic
      memapsin 2 inhibitor substrate analogue OM99-1
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<221> MOD_RES
<222> (3)..(4)
<223> Xaa at positions 3 and 4 represent Leu and Ala
      with the peptide bond substituted by a
      transition-state isostere hydroxyethylene
      (-CH(OH)-CH-2-) group
<400> 27
Val Asn Xaa Xaa Ala Glu Phe
                 5
  1
<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence:octapeptide
      upon which synthetic memapsin 2 inhibitor
      substrate analogue OM99-2 is based
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<400> 28
Glu Val Asn Leu Ala Ala Glu Phe
<210> 29
<211> 4
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence:retained
      structure of synthetic memapsin 2 inhibitor
      substrate analogue OM99-1 with outside subsites
      P4, P3, P3' and P4' discarded
<220>
<221> MOD RES
<222> (2)..(3)
<223> Xaa at positions 2 and 3 represent Leu and Ala
      with the peptide bond substituted by a
      transition-state isostere hydroxyethylene
      (-CH(OH)-CH-2-) group
<400> 29
Asn Xaa Xaa Ala
  1
<210> 30
<211> 10
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:synthetic
      peptide NCH-gamma
Val Gly Ser Gly Val Leu Leu Ser Arg Lys
<210> 31
<211> 326
<212> PRT
<213> Homo sapiens
<220>
<223> pepsin
<220>
<223> amino acids 2-5, 6-9, 13-20, 25-32, 65-67, 69-74,
      79-87, 89-91, 99-106, 119-122, 150-154, 164-167,
      180-183, 191-194, 196-199, 201-204, 210-214,
      221-223, 258-262, 265-269, and 275-278 are beta
      strands
<220>
<223> amino acids 281-284, 286-288, 298-301, 310-315,
      and 319-324 are beta strands
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- <220>
- <220>
- <223> amino acids 12-13, 30, 32, 34-35, 73-77, 111, 117,
  120, 189, 213, 215, 217-220, 287, 289, 291, 298,
  and 300 are residues in contact with pepstatin.
- <400> 31
- Val Asp Glu Gln Pro Leu Glu Asn Tyr Leu Asp Met Glu Tyr Phe Gly
  1 5 10 15
- Thr Ile Gly Ile Gly Thr Pro Ala Gln Asp Phe Thr Val Val Phe Asp 20 25 30
- Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Val Tyr Cys Ser Ser Leu 35 40 45
- Ala Cys Thr Asn His Asn Arg Phe Asn Pro Glu Asp Ser Ser Thr Tyr 50 55 60
- Gln Ser Thr Ser Glu Thr Val Ser Ile Thr Tyr Gly Thr Gly Ser Met 65 70 75 80
- Thr Gly Ile Leu Gly Tyr Asp Thr Val Gln Val Gly Gly Ile Ser Asp 90 95
- Thr Asn Gln Ile Phe Gly Leu Ser Glu Thr Glu Pro Gly Ser Phe Leu 100 105 110
- Tyr Tyr Ala Pro Phe Asp Gly Ile Leu Gly Leu Ala Tyr Pro Ser Ile 115 120 125
- Ser Ser Ser Gly Ala Thr Pro Val Phe Asp Asn Ile Trp Asn Gln Gly 130 135 140
- Leu Val Ser Gln Asp Leu Phe Ser Val Tyr Leu Ser Ala Asp Asp Gln 145 150 155 160
- Ser Gly Ser Val Val Ile Phe Gly Gly Ile Asp Ser Ser Tyr Tyr Thr 165 170 175
- Gly Ser Leu Asn Trp Val Pro Val Thr Val Glu Gly Tyr Trp Gln Ile 180 185 190
- Thr Val Asp Ser Ile Thr Met Asn Gly Glu Ala Ile Ala Cys Ala Glu 195 200 205
- Gly Cys Gln Ala Ile Val Asp Thr Gly Thr Ser Leu Leu Thr Gly Pro 210 215 220
- Thr Ser Pro Ile Ala Asn Ile Gln Ser Asp Ile Gly Ala Ser Glu Asn 225 230 235 240
- Ser Asp Gly Asp Met Val Val Ser Cys Ser Ala Ile Ser Ser Leu Pro 245 250 255
- Asp Ile Val Phe Thr Ile Asn Gly Val Gln Tyr Pro Val Pro Pro Ser 260 265 270

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Ala Tyr Ile Leu Gln Ser Glu Gly Ser Cys Ile Ser Gly Phe Gln Gly
        275
                            280
Met Asn Leu Pro Thr Glu Ser Gly Glu Leu Trp Ile Leu Gly Asp Val
                        295
Phe Ile Arg Gln Tyr Phe Thr Val Phe Asp Arg Ala Asn Asn Gln Val
                    310
                                        315
Gly Leu Ala Pro Val Ala
<210> 32
<211> 19
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:beginning of
      promemapsin 2 T1 and T2 construct
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Gly Val Leu
<210> 33
<211> 6
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: ending of
      promemapsin 2 T1 construct
<400> 33
Gln Thr Asp Glu Ser Thr
<210> 34
<211> 6
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: ending of
      promemapsin 2 T2 construct
<400> 34
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<210> 35
<211> 8
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<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:synthetic
      memapsin 2 inhibitor substrate analogue OM99-2
<220>
<221> MOD RES
<222> (4)..(5)
<223> Xaa at positions 4 and 5 represent Leu and Ala
      with the peptide bond substituted by a
      transition-state isostere hydroxyethylene
      (-CH(OH)-CH-2-) group
<400> 35
Glu Val Asn Xaa Xaa Ala Glu Phe
<210> 36
<211> 8
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:pro-memapsin 2
      hydrolytic site #1 (aa 12-18 of SEQ ID NO:3)
<400> 36
Arg Gly Ser Met Ala Gly Val Leu
<210> 37
<211> 8
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:pro-memapsin 2
      hydrolytic site #2 (aa 23-30 of SEQ ID NO:3)
Gly Thr Gln His Gly Ile Arg Leu
<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:pro-memapsin 2
      hydrolytic site #3 (aa 98-105 of SEQ ID NO:3)
Ser Ser Asn Phe Ala Val Gly Ala
  1
                  5
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<210> 39
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:pro-memapsin 2
    hydrolytic site #4 (aa 183-190 of SEQ ID NO:3)

<400> 39
Gly Leu Ala Tyr Ala Glu Ile Ala
    1    5
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- 60 × 10 x